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 GenCore version 5.1.3

on protein - nucleic search, using frame_plus_p2n model

Run on: November 9, 2002, 07:32:20 ; Search time 2740 Seconds
 (without alignments)
 2018.078 Million cell updates/sec

Title: US-09-895-298a-83

Perfect score: 190
 Sequence: 1 MNFQPPSKAWRASQMMTFF.....HDGSDLRRLRSRSVQEGNPPRA 190

Scoring table: OLIGO
 Xgapop 60.0 , Xgapext 60.0
 Ygapop 60.0 , Ygapext 60.0
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Word size: 4

Total number of hits satisfying chosen parameters: 2253933
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:
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 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB	ID	Description
1	190	100.0	1219	6 AX108540	AX108540 Sequence
2	190	100.0	1813	9 AK023655	AK023655 Homo sapi
3	190	100.0	1960	6 AX108538	AX108538 Sequence
4	190	100.0	2407	6 AX108534	AX108534 Sequence
5	190	100.0	2521	6 AX108536	AX108536 Sequence
6	190	100.0	2760	9 BC027602	BC027602 Homo sapi
7	135	71.1	2387	9 AK093944	AK093944 Homo sapi
8	126	66.3	2399	9 AK097718	AK097718 Homo sapi
9	59	31.1	220633	9 HUU91321	U91321 Human Chrom
10	35	31.1	223280	2 AC130456	AC130456 Homo sapi
11	12	13.2	110000	2 AC124442	AC003108 Human Chr
12	25	13.2	110000	10 MMU297000	MMU297000 Mus muscu
13	18	9.5	623	10 AC100377	AC100377 Mus muscu
14	17	8.9	71596	2 AX071021	AX071021 Sequence
15	16	8.4	402	6 AC100877	AC100877 Mus muscu
16	12	6.3	71596	2 AC100877	AC100877 Mus muscu
17	10	5.3	4790	1 SYTARABD	MJ1047 S. typhimurium
18	10	5.3	20558	1 AE008698	AE008698 Salmonella
19	10	5.3	91692	2 CNS08C9G	AL732641 Oryza sat
20	10	5.3	150789	9 HS21F7	AL033375 Human DNA
21	10	5.3	163876	2 AC094128	AC094128 Rattus no
22	10	5.3	170372	2 AC109276	AC109276 Mus muscu
23	10	5.3	190000	9 AF213884S1	AF213884 Homo sapi
24	10	5.3	193980	9 AC021120	AC021120 Homo sapi
25	9	4.7	330	6 AX135333	AX135333 Sequence
26	9	4.7	1534	1 EFU94356	U94356 Enterococcus
27	9	4.7	1949	8 AROARAH	L38853 Arachis hyp
28	9	4.7	12907	1 AE011768	AE011768 Xanthomon
29	9	4.7	28745	3 U00064	U00064 Homo sapi
30	9	4.7	76967	9 AC008475	AC008475 Homo sapi
31	9	4.7	88065	9 AP002045	AP002045 Homo sapi
32	9	4.7	94239	8 ATFP4P22	AL137082 Arabidops
33	9	4.7	95616	9 AC104655	AC104655 Homo sapi
34	9	4.7	99304	9 AC106825	AC106825 Homo sapi
35	9	4.7	107397	2 AP000612	AP000612 Homo sapi
36	9	4.7	110440	9 HS293E14	Z82900 Human DNA
37	9	4.7	110441	2 HS23	Z82169 Homo sapien
38	9	4.7	113116	2 AC094341	AC094341 Rattus no
39	9	4.7	115833	2 AC099324	AC099324 Oryza sat
40	9	4.7	116758	2 AP004134	AP004134 Oryza sat
41	9	4.7	120126	2 AC087096	AC087096 Oryza sat
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ALIGNMENTS

RESULT 2		RESULT 1	
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AK023655.1	AK023655.1	AK023655.1	AK023655.1
GI:10435644	GI:10435644	GI:10435644	GI:10435644
oligo capping; fis (full insert sequence).			
Homo sapiens	Homo sapiens	Homo sapiens	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 1219),			
Vinays Y de Bassols,C.			
Human tumor-associated polypeptides and their uses			
Patent: WO 0123417-A7 05-APR-2001;			
SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)			
Location/Qualifiers	Location/Qualifiers	Location/Qualifiers	Location/Qualifiers
1. .1219	1. .1219	1. .1219	1. .1219
/organism="Homo sapiens"	/organism="Homo sapiens"	/organism="Homo sapiens"	/organism="Homo sapiens"
/db_xref="taxon:9606"	/db_xref="taxon:9606"	/db_xref="taxon:9606"	/db_xref="taxon:9606"
BASE COUNT	346	346	346
ORIGIN	a	c	g
ORIGIN	a	c	t
Alignment Scores:		Alignment Scores:	
Pred. No.:	2.4e-189	Length:	1219
Score:	190.00	Matches:	190
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
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QY	1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe	QY	1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe
Db	4 ATGATGATTCCAGCTCCGAGAAAGCCTGGGGCCTCACAGATGATGACTTCTTC	Db	4 ATGATGATTCCAGCTCCGAGAAAGCCTGGGGCCTCACAGATGATGACTTCTTC
QY	21 IlePheLeuLeuPhePheProSerPheThrGlyValleuCysThrLeuAlaLeuLeuIle	QY	21 IlePheLeuLeuPhePheProSerPheThrGlyValleuCysThrLeuAlaLeuLeuIle
Db	64 ATCTTCTTGTCTCTTCCACCTTTCACCGGGCTCTGTCACCCCTGCCATCACCAC	Db	64 ATCTTCTTGTCTCTTCCACCTTTCACCGGGCTCTGTCACCCCTGCCATCACCAC
QY	41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHs	QY	41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHs
Db	124 TGGAGATGGAGCCTTCAGCTGAGCTGGCCCTTTCGAGGCTCAGCTCTTCATTCA	Db	124 TGGAGATGGAGCCTTCAGCTGAGCTGGCCCTTTCGAGGCTCAGCTCTTCATTCA
QY	61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp	QY	61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp
Db	184 TCCATCTACAGCTGGATGACACCTTAAGTACAGCCTGGCTACCTGTGGTTGG	Db	184 TCCATCTACAGCTGGATGACACCTTAAGTACAGCCTGGCTACCTGTGGTTGG
QY	81 IleTyrArgAsnLeuIleGlySerValHsPhePhePhePheIleLeuIleLeuIleLeu	QY	81 IleTyrArgAsnLeuIleGlySerValHsPhePhePhePheIleLeuIleLeuIleLeu
Db	244 ATCTATCGGAACCTCATGGAGCTGTCACCTTCACCCCTCATGGCTG	Db	244 ATCTATCGGAACCTCATGGAGCTGTCACCTTCACCCCTCATGGCTG
QY	101 IleLeuThrIleLeuIleLeuIleLeuIleLeuIleLeuIleLeuIleLeuIleLeu	QY	101 IleLeuThrIleLeuIleLeuIleLeuIleLeuIleLeuIleLeuIleLeuIleLeu
Db	304 ATCATCACCTATCTTACTGGCAGATCACAGAGGAAGGAGATATGATAAGGTGCTC	Db	304 ATCATCACCTATCTTACTGGCAGATCACAGAGGAAGGAGATATGATAAGGTGCTC
QY	121 HisGluGlnIleLeuAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys	QY	121 HisGluGlnIleLeuAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys
Db	364 CATGAGCAGATCATTAATGAGGCCAAAGATAAAATGTCCTGATAGAAAATTGATCAAG	Db	364 CATGAGCAGATCATTAATGAGGCCAAAGATAAAATGTCCTGATAGAAAATTGATCAAG
QY	141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal	QY	141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal
Db	424 CTGCAGGATACGAGAAAGCAACCCAGCTCAGTGTCTGGAAAGGAGAGGTG	Db	424 CTGCAGGATACGAGAAAGCAACCCAGCTCAGTGTCTGGAAAGGAGAGGTG
QY	161 GluGlnGlnGlyPheLeuIleLeuGlyGluIleAspGlySerLeuAspLeuArgSerArg	QY	161 GluGlnGlnGlyPheLeuIleLeuGlyGluIleAspGlySerLeuAspLeuArgSerArg
Db	484 GAGCAACAGCCTTTGCAATTGGGACATGAGCTTGTACTGGCATGAGCTG	Db	484 GAGCAACAGCCTTTGCAATTGGGACATGAGCTTGTACTGGCATGAGCTG
QY	181 ArgSerValGlnGluGlyAsnProArgAla 190	QY	181 ArgSerValGlnGluGlyAsnProArgAla 190
Db	544 AGATCAGTCAGAAGGTAATCCAAGGCC 573	Db	544 AGATCAGTCAGAAGGTAATCCAAGGCC 573

Db 511 ATCTCTGTCTTTCCTTCCATCTTCACCGGGCTCTGTGCACCCGGCCATCACCAC 570.

Qy 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheLeuHis 60

Db 571 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTCGAGGCTGCCCTTCATC 630

Qy 61 SerIleThrSerTriPleAspThrLeuSerThrArgProGlyTyLeuTrpValValTrp 80

Db 631 TCCATCTACAGCTGATCAGACACCTAAGTACACGGCCTGGCTACCGCTACTGTTGG 690

Qy 81 IleTyrrArgAsnLeuIleGlySerValHisPhePhePhePheIleLeuIleLeu 100

Db 691 ATCTATCGAACCTCATGGAAGTGTGCACTCTTCTATCCACCCCTCATGGCT 750

Qy 101 IleLeuThrTyLeuTyTrpGlnIleLeuIleLeuIleLeu 120

Db 751 ATCATCACCTACTTACTGGCAGATCACAGAGGAAGGAGATTATGATAAGGCTGCTC 810

Qy 121 HisGluGlnIleLeuAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuLys 140

Db 811 CATGAGCAGATCATTAACTGAGGCCAAAGATAAAATGTTCTGTAGATAAAATGATCAAG 870

Qy 141 LeuGlnAspMetGluLysAlaAsnProSerSerLeuValLeuGluArgGluVal 160

Db 871 CTGCAGGATATGGAGAAGAACCCACGCTCACTGTGTCGGAAAGGAGAGG 930

Qy 161 GluGlnGlnGlyPheLeuHisLeuGlyGluLysAspGlySerLeuAspLeuArgSerArg 180

Db 931 GAGCAACAAAGGCTTTCGATTTGGGGAAACATGATGGCAGTTGCGACTCTAGA 990

Qy 181 ArgSerValGlnGluGlyAsnProArgAla 190

Db 991 AGATCAGTCAAGAAGGTAATCCAAAGGCC 1020

RESULT 3

AX108538

LOCUS AX108538 1960 bp DNA linear PAT 30-APR-2001

DEFINITION Sequence 5 from Patent WO0123417.

ACCESSION AX108538

VERSION AX108538.1 GI:13923838

KEYWORDS

SOURCE

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 1960), Vinals Y de Bassols, C.

TITLE Human tumor-associated lak-4p related polynucleotides and polypeptides and their uses

JOURNAL Patent: WO 0123417-A 5 05-APR-2001; SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)

FEATURES source

1..1960 /organism="Homo sapiens"

BASE COUNT 515 a 439 c 447 g 559 t

ORIGIN

Alignment Scores:

Pred. No.: 3.54e-189 Length: 1960

Score: 190.00 Matches: 190

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-895-298A-83 (1-190) x AX108538 (1-1960)

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Qy 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrIleLeuThrIle 40

Db 805 ATCTCTGTCTTCCATCTTCACCGGGCTCTGTGCACCCGGCCATCACCAC 864

Qy 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheLeuHis 60

Db 865 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTCGAGGCTGCCCTTCATC 924

Qy 61 SerIleThrSerTriPleAspThrLeuSerThrArgProGlyTyLeuTrpValValTrp 80

Db 925 TCCATCTACAGCTGATCAGACACCTAAGTACACGGCCTGGCTACCGCTACTGTTGG 984

Qy 81 IleTyrrArgAsnLeuIleGlySerValHisPhePhePhePheIleLeuIleLeu 100

Db 985 ATCATCACCTACTGAGCTCATGGATCGAACCCCTAACAGTACACGGCCTGGCTACTCTGTTGG 1044

Qy 101 IleLeuThrTyLeuTyTrpGlnIleLeuIleLeuIleLeu 120

Db 1045 ATCATCACCTACTTACTGGCAGATCACAGAGGAAGGAGATTATGATAAGGCTGCTC 1104

Qy 121 HisGluGlnIleLeuAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuLys 140

Db 1105 CATGAGCAGATCATTAACTGAGGCCAAAGATAAAATGTTCTGTAGATAAAATGATCAAG 1164

Qy 141 LeuGlnAspMetGluLysAlaAsnProSerSerLeuValLeuGluArgGluVal 160

Db 1165 CTGCAGGATATGGAGAAGAACCCACGCTCACTGTGTCGGAAAGGAGAGG 1224

Qy 161 GluGlnGlnGlyPheLeuHisLeuGlyGluLysAspGlySerLeuAspLeuArgSerArg 180

Db 1225 GAGCAACAGGCTTTCGATTTGGGGAAACATGATGGCAGTTGCGACTCTAGA 1284

Qy 181 ArgSerValGlnGluGlyAsnProArgAla 190

Db 1285 AGATCAGTCAAGAAGGTAATCCAAAGGCC 1314

RESULT 4

AX108534

LOCUS AX108534 2407 bp DNA linear PAT 30-APR-2001

DEFINITION Sequence 1 from Patent WO0123417.

ACCESSION AX108534

VERSION AX108534.1 GI:13923834

KEYWORDS

SOURCE

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 2407), Vinals Y de Bassols, C.

TITLE Human tumor-associated lak-4p related polynucleotides and polypeptides and their uses

JOURNAL Patent: WO 0123417-A 1 05-APR-2001; SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)

FEATURES source

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BASE COUNT 635 a 557 c 546 g 669 t

ORIGIN

Alignment Scores:

Pred. No.: 4.19e-189 Length: 2407

Score: 190.00 Matches: 190

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Best Local Similarity: 100.00% Mismatches: 0

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Db 1192 ATGATGAATTCCAGCCTCCGAGCAAGCCTGGGGCCTCACAGATGACTTCTC 1251

QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaLalleThrile 40
 Db 1252 ATCTCTCTGCRCTTTCACCGGGCTCTGGCACCCCTGCCATCACCAC 1311
 QY 41 TpArgLeuLysProSerAlaAspCysGlyProPheArgLysLeuProLeuPheLeHis 60
 Db 1312 TGGAGATGAGCCTTCAGCTGACTGTGCCCTTCAGGCTCTGCCTCTTCATCAC 1371
 QY 61 SerIleTyrsrTpileAspThrLeuSerThrArgProGlyTyLeuTrpValValTrp 80
 Db 1372 TCCATCTACAGCTGGATGACACCTAAGTACAGGCCCTACCTGTGGTGTGG 1431
 QY 81 IleTyrsrArgAsnLeuIleGlySerValHisPhePhePheLeuThrLeuLeu 100
 Db 1432 ATCTATCGAACCTCATGGAAAGTGTGCACCTCTTCATCTCACCTCATGGCTC 1491
 QY 101 IleIleThrTyLeuTyTrpGlnIleThrGluGlyArgLysIleMetIleArgLeu 120
 Db 1492 ATCATCACCTATCTTACTGGCAGATCACAGAGGAGATTATGATAAGGCGCTC 1551
 QY 121 HisGluGlnIleLeuAsnGluGlyLysAspLysMetPheLeuIleGluLysLeu 140
 Db 1552 CATGAGCAGATCATTAAATGAGGGCAAGATTAATGTTCTGATAGAAATTCATCAAG 1611
 QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerIeuValLeuGluArgGlu 160
 Db 1612 CAGCAGGATATGGAGAAAGCAAAACCCAGCTCACTGTCTGGAAAGGAGAGGTG 1671
 QY 161 GluGlnGlnGlyPheLeuHisLeuGlyLysAspGlySerLeuAspLeuArgSerArg 180
 Db 1672 GACCAACAGGCTTTGCATTGGGAGACATGATGGCAGTCTGACTTGGCATCTAGA 1731
 QY 181 ArgSerValGlnGluGlyAsnProArgAla 190
 Db 1732 AGATCAGTTCAAGAAGGTAATCCAGGGCC 1761

RESULT 5
 AX108536

LOCUS AX108536 DEFINITION Sequence 3 from Patent WO0123417. DNA LINEAR PAT 30-APR-2001
 ACCESSION AX108536.1 GI:13923835
 VERSION 1
 KEYWORDS human.
 SOURCE
 ORGANISM
 REFERENCE 1 (bases 1 to 2521)
 AUTHORS vinal, Y de Bassols, C.
 TITLE Human tumor-associated lak-4p related polynucleotides and polypeptides and their uses
 JOURNAL Patent: WO 0123417-A 3 05-APR-2001;
 SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
 FEATURES source
 /organism="Homo sapiens"
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 BASE COUNT 662 a 583 c 583 g 693 t
 ORIGIN

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 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 6 Indels: 0
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US-09-895-298A-83 (1-190) x AX108536 (1-2521)

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QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaLalleThrile 40
 Db 1366 ATCTCTTGCTCTTTCACCGGGCTCTGGCACCCCTGCCATCACCAC 1425
 QY 41 TpArgLeuLysProSerAlaAspCysGlyProPheArgLysLeuProLeuPheLeHis 60
 Db 1426 TGGAGATGAGCCTTCAGCTGACTGTGGCCCTTCAGGAGCTGCTCTTCATCAC 1485
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 Db 1486 TCCATCTACAGCTGGATGACACCTAAGTACAGGCCCTACCTGTGGTGTGG 1545
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 QY 101 IleIleThrTyLeuTyTrpGlnIleThrGluGlyArgLysIleMetIleArgLeu 120
 Db 1606 ATCATCACCTATCTTACTGGCAGATCACAGAGGAGATTATGATAAGGCGCTC 1665
 QY 121 HisGluGlnIleLeuAsnGluGlyLysAspLysMetPheLeuIleGluLysLeu 140
 Db 1666 CATGAGCAGATCATTAAATGAGGGCAAGATAATGTTCTGATAGAAATTGATCAAG 1725
 QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerIeuValLeuGluArgGlu 160
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 QY 161 GluGlnGlnGlyPheLeuHisLeuGlyGluLysAspGlySerLeuAspLeuArgSerArg 180
 Db 1786 GACCAACAGGCTTTGCATTGGGGAGACATGATGGCAGTCTGACTTGGCATCTAGA 1845
 QY 181 ArgSerValGlnGluGlyAsnProArgAla 190
 Db 1846 AGATCAGTTCAAGAAGGTAATCCAGGGCC 1875

RESULT 6
 BC027602

LOCUS BC027602 DEFINITION Homo sapiens, Similar to RIKEN cDNA 4932443L08 gene, clone MGC:483911, mRNA, complete cds.
 ACCESSION BC027602
 VERSION BC027602.1 GI:20381190
 KEYWORDS MGC.
 SOURCE
 ORGANISM Homo sapiens.
 REFERENCE 1 (bases 1 to 2760)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbiology.org>
 contact: amadan@systemsbiology.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 34 Row: P Column: 13
 This clone was selected for full length sequencing because it

passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein.

FEATURES

source
1. 2760
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/clone="MGC:26648 IMAGE:4839111"
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213. . 2495
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/product="Similar to RIKEN cDNA 4932443L08 gene"

/db_xref="GI:20381191"

/translation="MLSDDHVNELLQEVNWSGGVOSHPSNSQIFQEKVLLDSINMVLSISDIDVSDQTSVSKRNDQKGQVLRFSTSLSMSMOTLHSLECMGIDTPGSSHETVOCOKLTLASLIPMTSRDKRAIRNQPRTMKERNLRSKQTHRILQNLNCIQLNISISRAVRRSKNSLSEILNISLWOKTLKILGGKFTGTSVLSYFNFLRWLKFENIFSFILNFSFLIPQFTVAKNTLQFTGLEFFTG/GYFRDTWVWYGFYTNSTIOHGNNSASYNMDQAVIIFTIGACLTCCFFLSMSAKYFRNNTNPHTYSGGITKLIFCWDFTVTHEKAVKLKOKNLSTEEIRENLSELRQNSKFLTNOLJTRFSAVMAVWVSTGVAIACCAVYVLAEVNLEFLKTHSNPGAVLVLPPFVUSCILNAYPCISMFRLVERYEMPRHEVFLRRIIGMQLTISLGLIQEFDIARNVLELIYQTLWIGIFFCPLPFIQIMLFLIMFYSKNISIIMNFEOPPSKAWRASQMMTEFIELFFPSTFVGVLTIAITIWRKPSADCGPFRGLPLFIMLISLYSWIDLTSTRPGYLWVWVWYRNLLGSHFFPFLITLIVLILITYWQITERKIMRLILHQEIQINEGKDKMFLIEKLKLQDMEKKANPSSLVLERREVEQQGFLHLGEHDGSDLDRRSRSVOEGNPR"

BASE COUNT 739 a 637 c 625 g 759 t

ORIGIN

Alignment Scores:

Score: 4.69e-189 Length: 2760

Percent Similarity: 100.00% Matches: 190

Best Local Similarity: 100.00% Conservative: 0

Query Match: 100.00% Mismatches: 0

DB: 9 0 Gaps: 0

US-09-895-298A-83 (1-190) x Bc027602 (1-2760)

Qy 1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20

Db 1923 ATGATGAAATTCCAGCCCTCCAGACAGATGACTTCTTC 1982

Qy 21 IlePheLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40

Db 1983 ATCTTCTTGCCTCTTCCCATCTTCACCGGGCTCTGGCACCCCTGCCATACCAC 2042

Qy 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60

Db 2043 TGGAGATTGAA GCCCTCAGCTGACTGTGGCCCTTCGAGGTCTGCCCTCTTCATC 2102

Qy 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyLeuTrpValValTrp 80

Db 2103 TCCATCTACAGCTGGATCGACACCTGATCACGGCCTGGCTACCTGGGGTGTGG 2162

Qy 81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleLeu 100

Db 2163 ATCTATCGGAACCTCATGGAACTGTCACCTCTTCTACCTCACCTCATGGCTA 2222

Qy 101 IleIleThrTyrLeuTyTrpGlnIleThrGluGlyArgLysIleMetIleArgLeu 120

Db 2223 ATCATCACCTATCTTACTGGAGATCACAGAGGGAAAGGAGATTATGATAAGGCTGCTC 2282

Qy 121 HisGluGlnIleLeuAsnGluGlyLysAspLysMetPheLeuIleGlyLysLeuIleLys 140

Db 2283 CATGAGCAGATCATTAATGAGGSCRAAGATAAATGTTCTGTAGAGAAATTGATCAAG 2342

Qy 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160

Db 2343 CTGCAAGGATATGGAGAAGAACCAAACCCAGCTCACTTGTCTCGAAAGGAGAGGTG 2402

Qy 161 GluGingLglyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180

Db 2403 GAGCAACAAAGCTTTGCAATTGGGGAGACATGATGCGACTTGCGATCTAGA 2462

Qy 181 ArgSerValGlnGluGlyAsnProArgAla 190

Db 2463 AGATCAGTCAAGAAGGTAATCCAAAGGCC 2492

RESULT 7

AK093944

Db 2343 CTGCAAGGATATGGAGAAGAACCAAACCCAGCTCACTTGTCTCGAAAGGAGAGGTG 2402

Qy 161 GluGingLglyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180

Db 2403 GAGCAACAAAGCTTTGCAATTGGGGAGACATGATGCGACTTGCGATCTAGA 2462

Qy 181 ArgSerValGlnGluGlyAsnProArgAla 190

Db 2463 AGATCAGTCAAGAAGGTAATCCAAAGGCC 2492

AK093944

59 cont. on 3/3/97

102(b)

QY 1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
 Db 1025 ATGATGAAATTCCAGCCTCGAGCAAGCCTGGGGCCTCGCAGATGATGACTTTC 1084
 QY 21 IlePheLeuLeuPhePheProSerSerPheThrGlyValuLeuCysThrLeuAlaLeuThrIle 40
 Db 1085 ATCTCTTGCTTTCCTTCACCGGGCTTGTGACCCCTGGCCATCACAC 1144
 QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleIle 60
 Db 1145 TTGGAGATGAGCTGGATCGACACCTTAAGTACAGGGCTGGTACCTGTGGGTTGG 1204
 QY 61 SerIleTrpSerTrpIleAspThrLeuSerThrArgProGlyTyrlLeuTrpValValTrp 80
 Db 1205 TCCATCTAGCTGGATCGACACCTTAAGTACAGGGCTGGTACCTGTGGGTTGG 1264
 QY 81 IleTrpArgLysAsnLeuIleGlySerValIlePhePheIleLeuThrLeuIleLeu 100
 Db 1265 ATCTATCGGAACCTCATGGAAAGTGTGACTTCTTTCATCTCACCCCATGGCTA 1324
 QY 101 IleIleThrIleTrpIleTrpGlnIleIleThrGluGlyArgLysIleMetIleArgLeuIle 120
 Db 1325 ATCATCACCTATCTTACTGGCAGACAGAGGAAGGATATGATAAGCTGCTC 1384
 QY 121 HisGluGlnIleLeuAsnGluGlyLysAspLysMetPheLeuIleGlu-LysLeuIleIle 140
 Db 1385 CATGAGCAGATCATTTATGAGGCCAAAGATAAAATGTTCCCTGATAGG-AAATTGATCAA 1443
 QY 140 SerGluGlnAspMetGluLysIleAsnProSerSerLeuValIleGluIargArgGlu 160
 Db 1444 GCTGCAGGATATGGAGAGAGAACCCAGCTCACTGTTCTGGAAAGGAGAGGT 1503
 QY 160 IGLuGlnGlnGlyPheLeuHisIleGlyGluHisAspGlySerLeuAspLeuArgSerIle 180
 Db 1504 GGAGCAACACAGGCTTTGCATTGGGGACATGATGCGACTTGACTTGCGATCTAG 1563
 QY 180 GargSerValGlnGluGlyAsnProArgAla 190
 Db 1564 AGATCAGTTCAAGAAGGGTAATCCAAAGGCC 1594
 RESULT 8
 AK097718
 LOCUS AK097718 2399 bp mRNA linear PRI 15-JUL-2002
 DEFINITION Homo sapiens cDNA FLJ40399 fis, clone TESTI2037081, weakly similar to Homo sapiens mRNA for LAK-4P.
 ACCESSION AK097718
 VERSION 1 GI:2175753
 KEYWORDS oligo capping; fis (full insert sequence); Homo sapiens; testis cDNA to mRNA, clone_lib:TESTI2
 SOURCE clone:TESTI2037081.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Oshima,A., Takahashi-Fuji,A., Tanase,T., Imose,N., Takeuchi,K., Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahashi,K., Masuho,Y., Nagai,K. and Isogai,T.
 TITLE NEDO human cDNA sequencing project
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2399)
 AUTHORS Isogai,T. and Yamamoto,J.
 TITLE Direct Submission
 JOURNAL Submitted (04-JUN-2002). Takao Isogai, FLJ Project(HRI Team); 2-6-7
 REFERENCE 1
 AUTHORS Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
 COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library
 FEATURES source
 BASE COUNT 610 a 591 c 528 g 670 t
 ORIGIN US-09-895-298A-83 (1-190) x AK097718 (1-2399)
 Alignment Scores:
 QY 1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
 Db 1933 ATGATGAAATTCCAGCCTGGAGCAAAGCCTGGGGCTCACAGATGATGACTTTC 1992
 QY 21 IlePheLeuLeuPhePheProSerSerPheThrGlyValuLeuCysThrLeuAlaLeuThrIle 40
 Db 1993 ATCTCTGCTCTTTCATCCATCCTCACCGGGCTTGTGACCCCTGGCCATCAC 2052
 QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleIle 60
 Db 2053 TTGGAGATGAGCTTCAGCTGACTTGTCAGCTGGCCATTGGAGCTGGCTCTCATC 2112
 QY 61 SerIleTrpSerTrpIleAspThrLeuSerThrArgProGlyTyrlLeuTrpValValTrp 80
 Db 2113 TCCATCTACACGGCTGGATGACACCTTAAGTACAGGGCTGGCTTACCTGTGGGTTGG 2172
 QY 81 IleTrpArgLysAsnLeuIleGlySerValIlePhePheIleLeuThrLeuIleLeu 100
 Db 2173 ATCTATCGGAACCTCATGGAAAGTGTGACTTCTGGCTTCTGGACCCATGGCTA 2232
 QY 101 IleIleThrIleTrpIleTrpGlnIleIleThrGluGlyArgLysIleMetIleArgLeuIle 120
 Db 2233 ATCATCACCTATCTTACTGGCAGACACAGGGAGGGAGGATATGATAAGGCCTGCTC 2292
 RESULT 9
 HU91321 HU91321 220633 bp DNA linear PRI 10-JAN-2000
 LOCUS HU91321
 DEFINITION Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.
 ACCESSION U91321
 VERSION U91321.1 GI:2951946
 KEYWORDS HTG.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Loftus,B.J., Kim,U.J., Sneddon,V.P., Kalush,F., Brandon,R., Fuhrmann,J., Mason,T., Crosby,M.L., Barnstead,M., Cronin,L., Deslattes,Mays,A., Cao,Y., Xu,R.X., Kang,H.L., Mitchell,S., Eichler,E.E., Harris,P.C., Venter,J.C. and Adams,M.D.
 COMMENT Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q
 TITLE Genomics 60 (3), 295-308 (1999)
 JOURNAL

ORIGIN

Alignment scores: 3.89e-50 Length: 220633

Pred. No.: 59.00 Matches: 59

Score: 59.00 Mismatches: 0

Percent Similarity: 100.00% Indels: 0

Best Local Similarity: 100.00% Gaps: 0

Query Match: 31.05% DB: 9

DB: 9

MEDLINE 99425270

PUBMED 10493829

REFERENCE 2 (bases 1 to 220633)

AUTHORS Adams,M.D., Loftus,B.J., Phillips,C.A., Zhou,L., Brandon,R., Fuhrmann,J. and Venter,J.C.

TITLE Direct Submission

JOURNAL Submitted (04-MAR-1997) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA

REFERENCE 3 (bases 1 to 220633)

AUTHORS Adams,M.D., Loftus,B.J., Zhou,L. and labombard,M.

TITLE Direct Submission

JOURNAL Submitted (21-MAY-1997)

REFERENCE 4 (bases 1 to 220633)

AUTHORS Adams,M.D., Loftus,B.J., Zhou,L., La Bombard,M., Kim,U.J. and Venter,J.C.

TITLE Direct Submission

JOURNAL Submitted (19-AUG-1997) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA

REFERENCE 5 (bases 1 to 220633)

AUTHORS Adams,M.D., Loftus,B.J., Zhou,L., La Bombard,M., Kim,U.J. and Venter,J.C.

TITLE Direct Submission

JOURNAL Submitted (22-AUG-1997) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA

REFERENCE 6 (bases 1 to 220633)

AUTHORS Adams,M.D.

TITLE Direct Submission

JOURNAL Submitted (11-MAR-1998) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA

COMMENT On Mar 11, 1998 this sequence version replaced gi:2335062.

BAC clone CIR987SK_363E6 is located in band 16p13.1 of chromosome 16. Genes were identified by a combination of five methods: XGRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (available by anonymous ftp from colin@u.washington.edu), GENSCAN (available using the e-mail server at genscan@genomic.stanford.edu), searches of the EST database at TIGR (<http://www.tigr.org/tdb/hcd/hcd.html>) and searches against a peptide database. Repeats were identified using RepeatMasker (Smit, A.F.A. and Green, P. unpublished, <http://ftp.genome.washington.edu/rm/RepeatMasker.html>).

FEATURES

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gene

mRNA

CDS

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BASE COUNT 61048 a 48977 c 49108 g 61449 t 51 others

US-09-895-298A-83 (1-190) x HU91321 (1-220633)

QY 42 ArgLeuLysProSerAlaAspCysGlyProProHeArgGlyLeuProLeuPhaLeuHisSer 61

Db 204986 AGATGAAGCCTCAGCTGACTGGCCCTTTCGAGGTcgcctCTCTCATCTACTCC 204925

QY 62 IleTyrSerTrpIleAspThrIleSerThrArgProGlyTyrLeuTrpValTrpIle 81

Db 204926 ATCTACAGCTGGATGACACCTAAGTACACGGCTGTGCTACCTGGGGTTGGATC 204985

QY 82 TyrArgAsnLeuIleGlySerValHisPhePhePhePheIleLeuIleLeuIleValLeu 100

Db 204986 TATCGGAACCTCATGGAAAGTGGACTCTTTCTATCCCTCACCCATGGCTG 205042

RESULT 10

AC130456

LOCUS AC130456 223280 bp DNA linear HTG 10-AUG-2002

DEFINITION Homo sapiens chromosome 16 clone CTA-363E6; WORKING DRAFT SEQUENCE, 5 unorderd pieces.

ACCESSION AC130456

VERSION AC130456.1 GI:22203229

KEYWORDS HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 223280)

AUTHORS DOE Joint Genome Institute.

TITLE Sequencing of Human Chromosome 16

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 223280)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL Submitted (10-AUG-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT -----Genome Center

Center Code: JGI

Web site: <http://www.jgi.doe.gov>

Project Information

Center Project Name: 2773242

Center clone name: CIR978SKA_363E6

Summary Statistics

Consensus quality: 221100 bases at least 040

Consensus quality: 222027 bases at least 030

Consensus quality: 222494 bases at least 020

Estimated insert size: 220633; agarose-fp estimation

Estimated insert size: 222880; sum-of-contigs estimation

Quality coverage: 10.81 in 020 bases; agarose-fp estimation

Quality coverage: 10.71 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 5 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 1261: contig of 1261 bp in length

* 1361: gap of unknown length

* 1362 2690: contig of 1329 bp in length

			ORGANISM	Mus musculus
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1		Tolstonog, G.V., Mothes, E., Shoeman, R.L. and Traub, P.	
AUTHORS			Isolation of SDS-Stable Complexes of the Intermediate Filament	
TITLE			Protein vimentin with Repetitive, Mobile, Nuclear Matrix Attachment Region, and Mitochondrial DNA Sequence Elements from Cultured Mouse and Human Fibroblasts	
JOURNAL			DNA Cell Biol. 20 (9), 531-554 (2001)	
PUBLMED	11747605			
REFERENCE	2	(bases 1 to 623)		
AUTHORS	Tolstonog, G.V.			
TITLE	Submitted (04-SEP-2000) Tolstonog G.V., Max-Planck-Institut fuer Zellbiologie, Rosenthal, Teltow/Heidelberg 68526, Germany			
JOURNAL			Location/Qualifiers	
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source			/organism="Mus musculus"	
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	AC124444_2	310000	Mismatches:	0
	AC124444_3	300001	Indels:	0
	AC124444_4	410001	Gaps:	0
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WPCOMMENT				
Sequence .split into 5 fragments		LOCUS	AC124444	Accession AC124444
Fragment Name		Begin		End
Db	1200	GAGGCCAAAGATAAAATGTTCTGTAGATAAAATTGATCAAGCTGCAGGATATGGAGAAG	1259	
QY	147	LysAlaAsnProSerSerLeuValLeuGluArgArgGluValGlu	161	
Db	1260	AAAGCAAACCCCAGCTCACTTGTCTGGAAAGGAGAGGGAGG	1304	
RESULT	12			
AC124444_2/c				
WPCOMMENT				
Sequence .split into 5 fragments		LOCUS	AC124444	Accession AC124444
Fragment Name		Begin		End
Db	1200	GAGGCCAAAGATAAAATGTTCTGTAGATAAAATTGATCAAGCTGCAGGATATGGAGAAG	1259	
QY	147	LysAlaAsnProSerSerLeuValLeuGluArgArgGluValGlu	161	
Db	1260	AAAGCAAACCCCAGCTCACTTGTCTGGAAAGGAGAGGGAGG	1304	
RESULT	12			
AC124444_2/c				
WPCOMMENT				
Sequence .split into 5 fragments		LOCUS	AC124444	Accession AC124444
Fragment Name		Begin		End
Db	1200	GAGGCCAAAGATAAAATGTTCTGTAGATAAAATTGATCAAGCTGCAGGATATGGAGAAG	1259	
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Db	1260	AAAGCAAACCCCAGCTCACTTGTCTGGAAAGGAGAGGGAGG	1304	
RESULT	12			
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WPCOMMENT				
Sequence .split into 5 fragments		LOCUS	AC124444	Accession AC124444
Fragment Name		Begin		End
Db	1200	GAGGCCAAAGATAAAATGTTCTGTAGATAAAATTGATCAAGCTGCAGGATATGGAGAAG	1259	
QY	147	LysAlaAsnProSerSerLeuValLeuGluArgArgGluValGlu	161	
Db	1260	AAAGCAAACCCCAGCTCACTTGTCTGGAAAGGAGAGGGAGG	1304	
RESULT	12			
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Fragment Name		Begin		End
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RESULT	12			
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WPCOMMENT				
Sequence .split into 5 fragments		LOCUS	AC124444	Accession AC124444
Fragment Name		Begin		End
Db	1200	GAGGCCAAAGATAAAATGTTCTGTAGATAAAATTGATCAAGCTGCAGGATATGGAGAAG	1259	
QY	147	LysAlaAsnProSerSerLeuValLeuGluArgArgGluValGlu	161	
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Fragment Name		Begin		End
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WPCOMMENT				
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Fragment Name		Begin		End
Db	1200	GAGGCCAAAGATAAAATGTTCTGTAGATAAAATTGATCAAGCTGCAGGATATGGAGAAG	1259	
QY	147	LysAlaAsnProSerSerLeuValLeuGluArgArgGluValGlu	161	
Db	1260	AAAGCAAACCCCAGCTCACTTGTCTGGAAAGGAGAGGGAGG	1304	
RESULT	12			
AC124444_2/c				
WPCOMMENT				
Sequence .split into 5 fragments		LOCUS	AC124444	Accession AC124444
Fragment Name		Begin		

Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
 Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
 Raymond,C., Rettig,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
 Roman,J., Roselli,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
 Seaman,S., Severi,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
 Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

COMMENT

TITLE

JOURNAL

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: L13918
 Center clone name: 35_B_17

* NOTE: This record contains 87 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

* 1 722: contig of 722 bp in length
 * 723 822: gap of 100 bp
 * 823 1526: contig of 704 bp in length
 * 1527 1626: gap of 100 bp
 * 1627 2336: contig of 710 bp in length
 * 2337 2436: gap of 100 bp
 * 2437 3156: contig of 720 bp in length
 * 3157 3256: gap of 100 bp
 * 3259 3984: contig of 728 bp in length
 * 3985 4084: gap of 100 bp
 * 4085 4811: contig of 727 bp in length
 * 4812 4911: gap of 100 bp
 * 4912 5638: contig of 727 bp in length
 * 5639 5738: gap of 100 bp
 * 5739 6477: contig of 739 bp in length
 * 6478 6577: gap of 100 bp
 * 6578 7305: contig of 728 bp in length
 * 7306 7405: gap of 100 bp
 * 7406 8107: contig of 702 bp in length
 * 8108 8207: gap of 100 bp
 * 8208 8950: contig of 743 bp in length
 * 8951 9050: gap of 100 bp
 * 9051 9743: contig of 693 bp in length
 * 9744 9843: gap of 100 bp
 * 9844 10583: contig of 740 bp in length
 * 10584 10683: gap of 100 bp
 * 10684 11405: contig of 722 bp in length
 * 11406 11505: gap of 100 bp
 * 11506 12236: contig of 731 bp in length
 * 12237 12336: gap of 100 bp
 * 12337 13070: contig of 733 bp in length
 * 13070 13169: gap of 100 bp
 * 13170 13851: contig of 682 bp in length
 * 13852 13951: gap of 100 bp
 * 13952 14685: contig of 734 bp in length
 * 14686 14785: gap of 100 bp
 * 15513 15612: gap of 100 bp

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	8.42%	Indels:	0
DB:	6	Gaps:	0
US-09-895-298A-83 (1-190) x AX071021 (1-402)			
QY	1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMet	16	
DB	 269 ATGATGAAATTCCACGCTCCGAGCAAAGCTTGGGGGCTCACAGATG	316	

Search completed: November 9, 2002, 08:33:48
Job time : 2869 secs

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* 45977 46076: gap of 100 bp
* 46077 46808: contig of 732 bp in length
* 46809 46908: gap of 100 bp
* 46909 47613: contig of 705 bp in length
* 47614 47713: gap of 100 bp
* 47714 48431: contig of 718 bp in length
* 48432 48531: gap of 100 bp
* 48532 49280: contig of 749 bp in length
* 49281 49380: gap of 100 bp
* 49381 50139: contig of 759 bp in length
* 50140 50239: gap of 100 bp
* 50240 50966: contig of 727 bp in length
* 50967 51066: gap of 100 bp
* 51067 51797: contig of 731 bp in length
* 51798 51897: gap of 100 bp
* 51898 52632: contig of 735 bp in length
* 52633 52732: gap of 100 bp
* 52733 53448: contig of 716 bp in length
* 53449 53548: gap of 100 bp
* 53549 54266: contig of 718 bp in length
* 54267 54366: gap of 100 bp
* 54367 55107: contig of 741 bp in length
* 55108 55207: gap of 100 bp
* 55208 55927: contig of 720 bp in length
* 55928 56027: gap of 100 bp
* 56028 56757: contig of 730 bp in length
* 56758 56857: gap of 100 bp

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Pred. No.: 1.7e-06 Length: 71596
 Score: 17.00 Matches: 17
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 8.95% Indexes: 0
 DB: 2 Gaps: 0

US-09-895-298A-83 (1-190) x AC100877 (1-71596)

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LOCUS AX071021 **402 bp** **DNA**
DEFINITION Sequence 1493 from Patient W00102568.
ACCESSION AX071021
VERSION AX071021.1 **GI:12581294**

Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi
 Mammalia; Eutheria; primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 402)
 AUTHORS
 Williams, L.R., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.,
 Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D.,
 Lamson, G., Drmanac, R., Crkenjakov, R., Drmanac, S., Dickson, M.,
 Labat, I., Leshkowitz, D., Kita, D., Garcia, V. and Strache-Crain, B
 TITLE
 Human genes and gene expression products
 JOURNAL
 Patent: WO 0102568-A1 1493 11-JAN-2001;
 CHIRON CORPORATION (US); HYSEQ, INC. (US)
 FEATURES
 Location/Qualifiers

BASE COUNT	83 a	106 c	87 g	124 t	2 others
/note="n = A,T,C or G"					

Alignment Scores: 2.75e-07
Pred. No.: 16.00
Score: 16.00
Length: 402
Matches: 16

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